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OM protein - protein search, using sw model

April 24, 2002, 10:36:32 ; Search time 120-27 Seconds Pun on:

(without alignments) 195,808 Million cell apdates/soc

102-17-4455-5664-554-60-80

CSNCKKSLPCTKLCLPQ18N 151 941 1. DSVCPQGKYTHP2NNSTPCT ritle: Perfect score: Sequence:

BLOSHM62 Gapop 10 0 , Gapext O S Scoring table:

473505 Total number of hits satisfying chosen parameters:

473505 soys, 146272329 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing lirst 45 summaries

SPTREMBL_17:*
: sp_archea:*
: sp_bacteria:* Database :

sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_invertebrate:* sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:* sp_mammal:* sp_mhc:* sp_fungi:* sp_human:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result. No.	Score	Query Match	" Query Match Length DB	DB	ID	Description
-	756	80.3	580	ء ع	047530	O97530 canis famil
2	731	77.7	189	ت	095185	095185 felis silve
	202	21.5	£ + 7		C99MM1	099mml mus muse:
4	200.5	21.3	147	, , ,	COERES	
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80	198.5	21.1	141	Ξ	QQER62	Q9er62 mus musculu
5	198.5	21.1	180	11	Q9C2A4	Q9cza4 mus musculu
10	SEE	7.1	417	4	очитив	Quby86 homo sapien
11	198	21.0	277	4	014865	
12	198	21.0	426	₹*	014865	014865 homo sapien
13	196	20 8	175	₹-	QQIIMPF	
14	196	20.8	178	4	09UME0	рошо
15	196	20.8	181	4	QSUME1	O9umel homo sapien
16	193	20.5	387	=	Q9PVD4	09pvd4 xenopus lae
17	188	20.0	302		OBEUSO	Sports Salvelinus
18	182.5	19.4	285	7	Q9DGH7	Q9dqh7 qallus qall
61	18.	2.5	417	·	5,40 M 1	. 12.3. F 2.1 TWO P.O.

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5.62	176.5	126	175.5	175.5	6.171	171.5	υ: [-]	171.5	100	168	a).	167.5	4:7	167.5	167.5	167	167	166.5	166.5	166 5	166.5	166	165	164.5	164.5
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ALIGNMENTS

RESULT 1 097530 DO 097530 DD 097530 DT 01-MAY-1999 (IFFMHLTC) 10 DT 01-MAY-1999 (IFFMHLTC) 17 DE TUMNS NECROSIS FATTOR RECE OS Canis familiaris (Dos). OS Canis familiaris (Dos). OS Canis familiaris (Dos). ON USB 1 AxiD=9615; NCB 1 AxiD=9615; NC
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EMBL; AF329969; AAK11256.1; -.
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                                                                                                                                                                                                                     413 AA;
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103 SKCRKEMNOVEISPCTVYRDTVCGCRKNOYRFYWSETLFQCNNCSLCLNGTVQISCQEKQ 162
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Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Musimae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Carnivora, Fissipedia, Felidae; Felis.
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MEDIINE-21158384; PubMed 11261933;
Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oucry Match 77.7%; Score 731; DB 6; Length 189;
Hest Local Similarity 85.5%; Pred. No. 1.7e 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duthie S., Nasir L., Eckersall P.D.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 189 180 MW: F3FBEDYEROGD7ERE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1997 (TrEMBLrel. 02, Created)
01-JUN-1998 (TrEMBLrel. 06 Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOUR NECHOSIS FACTION PROPERTY PAGE (FRACMENT).
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01-JUN-2001 (TERMELFEL 17, Last annotation update)
WSL-1-LIKE PROFERN.
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                                                                                                            123 NTVCTCHAGFFLRENECVSCSNCKKS 148
                                                                                                                                                                           163 NTICTCHAGFFLREHECVSCVNCKKN 188
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ProDom; PD000771; TNFR_C6; 1.
SMAPT; SM00208; TNFR; 3.
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SIGNATE 2.29. PubMed 11063728; Bogemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R., Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R., Lane N., Reik W., Walter J.; Segmence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting."; Hum. Mol. Genet 9:2691-2706(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 CIVDRDIVGGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSC------QEKQNTVCT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 CSAKSDIHGGGQSG----W-----CVDCSTVPGGKSSPFSCVPGGAITPVHEAPTPRP 162
                                                                                                                                                                                                                                                                                                                                                                                       28, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GTTKGHKGTYLYNDGPGPGGDTDGPBGBSGSFTASENHLM-HGLSGSKGRKEMGGVEISS 76
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Owen M.J.;
"Genomic structure, expression, and chromosome mapping of the mouse
homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eskaryeda, Metalea, Chordata, Craniata, Vertebrata, Eutelecatomi,
Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                            21.5%; Score 202; DB 11; Length 413; 31.4%; Pred. No. 2.6e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, A.278264; CAC16405.1; -.
EMBL; AJ276505; CAC27852.1; -.
EMBL; AJ276505; TALFSTIALL
INTEPPROF : PRE00345; Cytc. heme_bind.
InterPro; IPR00345; Cytc. heme_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus domesticus (western European house mouse).
                                                                                                                                                                                                             44453 MW; 69F21B85D0DABABF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 AA; 16253 MW; 7644271340517DC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last Sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   , B
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(09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR NECKUSIS FACTOR RECEPTOR PEOPLOGOUS TINERSFIALL OR THERHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16, Mismatches
                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 CHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PSOULAD, CYTOCHFOME_C; UNKNOWN_1
PPOSITE; PSSCOSO; TNPP_NSPP_2; 2.
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64 KORKEMGOVETSSCTVOPPTTVGGGRKNQYEHYWSENLEGGENOSLGLNG-TVHLSCQEKÇ 122
                   70 GQVEISSCTVPRPTVCGCRENQFRFWSENLFQC----FNCSLCLN-GFVH----LSCQ_119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 SQVALENCSAVADIFOGOKFGWEVEC---QVSQCVSSSPFYCQPCLDCSALHKHTELLCS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDIFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 HPQNNSIGCTKCHKGHYLYNDCPGPGQDTDCRECESGSFTASENHLR HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota: Metamoa; Ckordata; Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota: Metasca, Chordata, Craniata; Vertebrata, Euleleostomi,
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "LARD: a new lymphoid-specific death domain containing receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cuery Match 21.3%: Score 200.5; DB 4; Longth 253, Best Local Similarity 29.8%; Pred. No. 2.5e-13; Matches 48; Conservative 20; Mismatches 72, Indels 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Screaton G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R., McMichael A.J., Bell J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00208; TNFR; 2.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS0052: INFR_NGFR_1; 2.
PROSITE; PS0050; TNRR_NGFR_2; 1.
SP2UTENCE 253 AA; 26934 MM; 4CD06775B68E9292 CR054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel 17, Last annotation update)
                                                                                                                                                                                                                                                   01-30L-1997 (TrEMBLrel. 04, Last sequence update)
01-30N-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 RRDIDGGTGLPGFYEHGDGCVSCPISILGSGPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulated by alternative pre mRNA splicing.",
Proc. Natl Arad. Sri H S A 94:4615-4619(1997).
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                                                                                                                                                                                                                                                                                              LYMPHOCYTE ASSOCIATED PPCPPTOR OF DEATH 2.
                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                         MPPLINE-97272273; PubMed-9114039;
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InterPro: IPR001368; INFE_c6.
Pfam: PF00020; INFE_c6: 2
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HSSP; P19438; 1EXT.
                                                                                                                                                                                                    PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELLIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9606;
                                                                    123 NTVCT 127
                                                                                                         123 NTVCS 127
                                                                                                                                                                                                                      000276;
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SHOUENCE FROM N.A.

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70 GOVELLSSCIADAFITYCGCRKNGFRHYMSENEFOG-----PINGSECEN-GIVH----ESCQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zl; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 HPQNNSICCIRCHKGIYLYNDCPGPGQOINTRECESGSFIASFNHLP-HOLSGSFOPKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 HKKIGLEGTPRÖPAGBYLKAPTIEPTANSFTLYTPLOTFLAMENHINSETARGGAGDEGA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Graniata, Vertebrata, Eufeleostomi,
Mammalia, Eutheria, Primates, Catarihini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MINITAL-97272273; PubMed 9114089; Screeton G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R., McMichael A.J., Bell J.L., Bell J.L., Bell D.L., Compared a proposition of the second specific death domain containing receptor requiated by alternative pre-mRNA splicing."; Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997). HSRP; P19438: 1EXI.
MEDLINE 97272273; PubMcd 9114039; Screetin G.E., Xu.X.N., visen A.L., Compor A.E., Tan E., McMichael A.J., Bell J.T.; McMichael A.J., Bell J.T.; McMichael A.J., Bell J.T.; McMichael A.J., Bell J.T.; McMichael B.J., Bell J.T.; McMichael B.J., McMichael B.J., Bell J.J., McMichael B.J., M
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                                                                                                                                                                                                                                                                                                                                                                                                       FIGHT PRODUCT: INFECE; 2.
SMART: SM00005: DEATH: 1.
SMART: SM00005: TNFR: 1.
PROSITE: PS50017: DEATH: DOMAIN: 1.
PROSITE: PS01186: ESF_2: DNRNOWN_1.
FROSITE: PS01186: ESF_2: DNRNOWN_1.
FROSITE: PS00052: TRFR_NOTE: 1.
SECUENCE: 3800 AA: 41192 MM: EALISHSB6AAD947H7 CRC64;
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01-JUN-2001 (TERMBLEEL, 17, Last annotation update)
LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 EKONIVOLOHAGIILRENEAVSC SNORKSLECIKLO 155
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PROSITE: PS01186; EGE_2; UNKNOWL.1.
PRUSITE: PS00462; INFR_MSFE_1, 2.
PRUSITE: PS50050; INFR_MGFE_2; 1.
SEQUENCE: 418 AA; 45456 MM; 5484
                                                                                                                                                                                                                                                                                                            InterPro; IPR000561; EGF-like.
InterPro; IPR001368; INFR_c6.
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InterPro: IPR001368; INFR_c6.
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                                                                                                                                                                                                                                                                        InterPro; IPR000488; Death.
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SMART, SM00005, DEATH; 1.
SMART, SM00208; INFR; 2.
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                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00531; death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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123 NTVCS 127

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                                                                                                                                                                                                                                                                                                 70 GOVEISSCIVDPPIVEGFRNGYPHYWSENLFG******FN*SLYLN*GTVH*****LSCQ_119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 KÜRKEMMODVETSSCTVINPITTVOGPRINAPHYMSENLEGGENGSLOLING-TVHLSOQEKQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 HPONNSTOCTKCHKGTYLYNDCPGPGQUTDCKECESGSFTASENHLR-HCLSCSKCKKEM 69
                                                                                                                                                                                                                       40 HKKIGLECCROCPAGHYLKAPCTEPCGNSICLVCPQDFFLAWENHINSBCARCQACDBQA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4. CPQCKYTHPQNNSTOCTKCHKGTYLYNDCPGPQDTDCPFCESGSFTASENHLPHCLSCS 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rukaryota, Mctazoa, Chordatu, Chariata, Vertebrata, Buteleustomi,
Mammalia, Eutheria, Rodentia. Seiurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
Lane N., Reik W., Walter J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.1%, Score 198.5; DB 11; Length 141; 32.8%; Prcd. No. 2.5c 13;
       DB 4; Length 418;
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus domesticus (western European house mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö9ER62;
01-MAP-2001 (TYEMBLYEL: 16, Last sequence update)
01-MAP-2001 (TYEMBLYEL: 16, Last sequence update)
01-JUN-2001 (TYEMBLYEL: 17, Last annotation update)
TUMOP NETPOSIS PATTOP PEREPTOP PAD HOMOLOGIE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 EKQNTVCTCHAGFFLRENECVSC - SNCKKSLECTKLC 155
21.3%; Score 200.5; DB 4; 29.8%; Pred. No. 3.7e-13; ttive 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000345; Cytc_heme_bind.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20519229; PubMed-11063728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38
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EMBI: AJ276505: CAC27353.1; -.
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SMAPT; SM00208; TNFP; 3.
                                                                             48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCB1_Tax ID-10092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MG1:1930270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-129 SV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Engemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41,
   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 CPAGEY----WSKDVCCKNCSAGTFVKAPCETPHTQGQCEKCHPGTFTEKDNYLDACILCS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 KCKKEMGQVE1SSCTVDRL/TVCGCRKNQYRHYWSENI,FQCFNCSI,CI,NG-TVHI,SCQEKQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4. CPQCKYTHPQNNSTCCPKCHKGTYLYNDCPGPGQDTDCKKCESGSFTASENHLRHCLSCS-63.
                                                                                                                                                                      Eukarycta, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.1%; Score 198.5; DB 11; Length 180; Best Local Similarity 32.8%; Pred. No. 3e-13; Aatches 41; Conservative 18, Mismatches 59, Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 AA; 20226 MW; F8F56F165ADD53FA CRC64;
                                         or conversed (TrEMBLrel, 17, Last sequence update) 01-JUN-2001 (TrEMBLrel, 17, Last annotation update) TNFRARIA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59,
    180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PET; 417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRESITE, FSOOTGO, PYTOCHFORE, PRINCOMAL, PROSITE, PSSOOSO, THER_NGER_2, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000345; Cytc heme_bind.
InterPro; IPR001368; TNFR_c6.
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01-JUN-2001 (TrEMHLrel, 17, Created)
    PRT;
                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE-EMBRYO;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1930270; Infrsflal2.
                                                                                                                                   TNFKSF1ALZ OR ZBIÖÖZBKÖĞRIK.
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EMBL, AK012838, BAB28502.1,
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  PRELIMINARY;
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                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                SHOUFINCE FROM N.A.
                                                                                                                                                                                                                     NCB1_Tax1D-10090;
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                         09C2A4;
09CZA4
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SMAKE; SM00005; DEATH; 1.
SMAKE; SM00208; INFR; 2.
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                                                                                                                                                                                     PRELIMINARY;
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01-JUN-2001 (TremBerel.
                                                                                                                                                                                                                                                               DEATH RECEPTOR 3 BETA.
                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 47; Conserva
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         NCB1_faxID=9606;
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                                                                                                                                                                                                    014865;
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                                                                                                                                                                                    014865
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                                                                                                                                                       RESULT 12
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                                                                                                                                                                                                                                                                                                                         21, Cars
                                                                                                                                                                                                                                                                                                                                                      11 HPQNNSIGGTKGHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HGLSGSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 HKKIGLEGTPGTPAGHYLKAPGTEPGGNSTGLVGPQDTFLAWENHUNSEGARGQAGDEGA 99
                                                                           Eukaryota, Metazoa, Chordata, Craniata, Virtebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryola, Motazoa, Chordata, Craniata, Vertebrata, Eutelwostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                         21.1%; Score 198.5; DB 4; Length 417;
29.8%; Prod. Mc. 6e-13,
tipe 20, Mismatches 72, Indels 21,
                                                                                                                                                    Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto H., Hayashi S., Sato M., Shiozawa K., Tsukamoto Y., "DR3 genome.";
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                  Submitted (NOV-2000) to the EMNL/GenBank/DDBJ databases
                                                                                                                                                                                                                                              417 AA; 45326 MW; 522631206D846619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3D19F3E847BFC093 CRC64;
01-JUN-2001 (IrEMBLrel. 17, Last sequence update) 01-TUN-2001 (TrEMBLrel 17, Tast appointing update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 EKQNTVOTOHAGEFLPENEOVSO----SNOKKSLEOTKLO 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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01-TAN-1998 (TrEMELFA) 05, Last sequ
01-JUN-2001 (TrEMBLEE). 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS01186; EGF_2: UNKNOWN_1. PROSITE: PS00652; TNFR_NGFR_1; 2. PROSITE: PS50050; TNFR_NGFR_2; 1. SEQUENCE 277 AA; 29111 MW; 3D19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001368, INFR_06.
                                                                                                                                                                                                         EMBL; AB051851; BAB40663.1;
Receptor.
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HSSP; P19438; 1NCF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Conservative
                                                                                                                                                                                                                                                                                                                        Conservative
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                                                              Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                     SECUENCE FROM N.A.
                                DEATH RECEPTOR 3.
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                                                                                                          NCBI_TaxID-9606;
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30
                                                                                                                                                                                                                                              SECUENCE
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Matches
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FRUSLULN-GIVH----LSCQ 119
                                   11. HOGNNSTOCKFORKSTYLVNIKOPOQUITIOPERSOSETASENHUR-HOUSOSKORKER 69
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Marzocha K., Ribeiro P., Charlot C., Renard N., Coiffier H.,
Sallos G.;
"A new death receptor 3 isoform, expression in human lymphoid cell
lines and non-Bedakin's Lymphomas.";
Blochem. Biophys. Res. Cymphomas.";
EMBL: AFQ2E970; AAC39556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bokaryota, Mctazca, Chordata, Craniata, vertebrata, Luteicostomi;
Masmalia, Batheria, Frimates, Catarrhini, Bominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.0%; Score 198; DB 4; Length 426; 31.3%; Pred, No. 6.9e-13; Live 17; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371AA7F16AD29C16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (ITEMBLIC), 13, Created)
U-MAY-2000 (ITEMBLIC), 13, Last sequence update)
01 JUN 2001 (ITEMBLIC), 13, Last annotation spoate)
DEATH DOMAIN REVEPTOR 3 SOLUBLE FORM (FRAGMEN),
                                                                                                                                                                                                                                                                                                                                                                                                                          05, Last sequence update)
17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRT, 175 AA.
70 CQVEISSCIVEREIVCSCRKNQYRHYWSENLFUC
                                                                                                                   120 ERQNIVITHAGEFLRENETVSUSNIKKSE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 ERGNIVOTOHASFFLRENECVSOSNOKKSL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 RRDIDCGTCLPGFYEHGDGCVSCPTPPPSL 186
                                                                                                                                                                            157 RRDIDCGICLPGFYENGDGCVSCPIPPPSL 186
                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel, 05, Created)
                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS50017; DEATH_DOMAIN: 1.
PPOSITE: PS01186: ESE_2: THENOWN_I
PPOSITE: PS00565; TNPP_NSFE_1; 2.
PROGUENCE: 426 AA: 45950 MME_2; 373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P19438; INCF.
InterPro; IPR000488; Beath.
InterPro; IPR000561; EGF-11Ke.
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Piam; PF00531; death; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 HPQNNSICCTKCHKGTYLYNDCPGPGQDYDCREGESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 HKKLIGLEGGRGCPACHYLKAPPCTEPCONSTCLVCPDFTTAWENHHNSECARCQACDEQA 93
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota: Metacoa, Chordata. Cramiata. Vertebrata. Futeleustumi,
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screaton G.R., Xu X.N., Oisen A.L., Cowper A.E., Tan R., McMichael A.J., Bell J.L.;
"LARD: a new lymphold-specific death domain containing receptor regulated by alternative pre-mRNA splicing.";
Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
HSSP; P19438; LEXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.8%; Score 196; DB 4; Length 175; 31.5%; Pred. No. 5.4e-13; Live 17; Mismatches 67; Indels
                                                                                                                                                Chaudhary P.M., Hood L.E.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U83598; AAB41433.1; -.
HSSP; P19438; 1EXT.
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01-MAY-2000 (TrEMBLECL 13, Last soquence update)
01-JUN-2001 (TrEMBLECL 17, Last annotation apdate)
LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 11 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 175 AA: 18634 MW; AE46876756832157 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT:
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                                                                                                                                                                                                                                                                                                                                                 SMAPT: SMONDAR: TNFE: 2
PROSITE; PSO1186; EGF_2; UNKNOWN_1.
PROSITE; PSO0552; TNFE_NGFE_1; 2
PROSITE; PSSON50: TNFE_NGFE_2; 1.
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                                                                                                                                                                                                                                                          InterPro; IPR000561; PGF-like.
InterPro; IPR001368; TNFE_GG.
Plam: PF00020; TNFE_GG; 2.
SMAPT: SMON208; TNFE_Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Conservative
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Matches 45; Conserva
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                                                                                                                                SEQUENCE FROM N.A.
                                                                            NCB1_Tax1D-9606;
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NON PER
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 GÜVETSSCTVDRDFVOSCHKNQYRHYWSENLFDC----FNCSLCLN-GTVH----LSCQ-119
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                                                                                                                        11 HPQNNSICCIKCHKGTYLYNDCPGPGQOTGYPRCESGSFTASENHLR-HCLSCSKCPKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 HEQNNSTOOTKOHKGTYLYNIX)PGPGQDTDCRECESGSFTASENHLR-HOLSOSKORKEM 69
                                                                                                                                                                                 37 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing,";
Proc. Natl. Arad. Sci. II S. A. 94.4615-4619(1997).
EMBL; U94505; AAC51310.1; -..
         20.8%; Score 196; DB 4; Length 178; 31.5%; Pred. No. 5.5e-13; Pred. 17, Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 20.8%; Score 196; DB 4; Length 181; Best Local Similarity 31.5%; Pred. No. 5,5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97272273; PabMed-9114039;
Screaton G R , Xu X N., Olsen A L., Cowper A F , Tan R ,
MeMichael A.J., Bell J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AA; 13432 MW, 59AAFELBBB46E369 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AA.
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Job time: 617 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ©90ME1;
01 MAY 2000 (TrEMBLrel. 13, Created)
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PPGSTTE; PS01186; DSF_2; UNKNOWN_1.
PPGSTTE; PS0055; 1NFK_NGFK_1; 2.
PPGSTTE; PS60055; 1NFK_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                      120 EKQNIVCTCHAGFFLRENECVSC 142
                                                                                                                                                                                                                                                                                                                                                                                                                154 RRDTDCGTCLPGFYEHGDGCVSC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 EKONTVCTCHAGFFLRENECVSC 142
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InterPro; IPR001368; INFR_c6.
Query Match
Hest Local Similarity 31.5%
Matches 45, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plam; PF00020; TNFR_C6; 2.
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